

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Kathleen L. Horwath et al.

Examiner:

Serial No.: (not yet assigned)

Group No.:

Filed: June 7, 2001

Date: June 7, 2001

Title: NUCLEIC ACID SEQUENCES ENCODING TYPE III TENEBRIO
ANTIFREEZE PROTEINS AND METHOD FOR ASSAYING ACTIVITY

Assistant Commissioner for Patents
Washington, D.C. 20231

SUBMISSION OF "SEQUENCE LISTING"
AND COMPUTER READABLE COPY

Sir/Madame:

Submitted herewith are:

A. "Sequence Listings" for the nucleotide and/or amino acid sequences in this application, each "Sequence Listing" is assigned a separate identifier as required in 37 CFR Sections 1.821(c) and 37 CFR Sections 1.822 and 1.823;

B. A copy of each "Sequence Listing" submitted for this application in computer readable form in accordance with the requirements of 37 CFR Sections 1.821(e) and 1.824;

C. The following statement that the content of each "Sequence Listing" submitted and each computer readable copy are the same as required in 37 CFR Section 1.821(f).

I hereby state that the information recorded in computer readable form is identical to the written sequence listing.

007640-0000

Respectfully submitted,

By: _____

Mark Levy
Reg. No. 29,188
Attorney for Applicants
SALZMAN & LEVY
Press Building, Ste. 902
19 Chenango St.
Binghamton, NY 13901

CERTIFICATE OF EXPRESS MAILING

09876348-060704
T02050-84E32868

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Horwath, K. L. et al.
- (ii) TITLE OF INVENTION: Nucleic Acids Sequences Encoding Type III Tenebrio Antifreeze Proteins and Method for Assaying Activity.
- (iii) NUMBER OF SEQUENCES: 48
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSEE: Dr. Kathleen L. Horwath
 - (B) STREET: Department of Biological Sciences, Binghamton University
 - (C) CITY: Binghamton
 - (D) STATE: New York
 - (E) ZIP: 13902-6000
- (v) COMPUTER READABLE FORM
 - (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 - (B) COMPUTER: IBM AT/ATX compatible
 - (C) OPERATING SYSTEM: Windows 95/98
 - (D) SOFTWARE: Microsoft Word
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
 - (A) APPLICATION NUMBER: 60210446
 - (B) FILING DATE: June 8, 2000
- (viii) ATTORNEY/AGENT INFORMATION
 - (A) NAME: Mark Levy, Attorney-at-Law
 - (B) REGISTRATION NUMBER: 29,188
 - (C) REFERENCE/DOCKET NUMBER: RB125
- (ix) TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE: 607-722-6600
 - (B) TELEFAX: 607-724-2207

09676348-060704

(2) INFORMATION FOR SEQ. ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE:

(ix) FEATURES:

- (D) OTHER INFORMATION: N-terminal sequence of protein Tm 12.86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val
 1 5 10 15

09676340-060704
 T02090-04092960

(2) INFORMATION FOR SEQ. ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Non-his-tagged, signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

GTGGATCCAA AGAATTCGGC ACGAGACTAC TAAG ATG AAG TTG CTC      36
                               Met Lys Leu Leu
                               -15

TGT TGT CTA ATC TCC CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG      81
Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu
                               -10                               1
                               -5

ACC GAG GCA CAA ATT GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT      126
Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys
                               5                               15

CAA AAT GAA AGT GGA GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC      171
Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg
                               20                               25                               30

AAC GGT GAC TGG GAG GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT      216
Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe
                               35                               40                               45

TGC GTG GCC AGG AAC GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG      261
Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val
                               50                               55                               60

GTG GTC GAC GTG TTG AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC      306
Val Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn
                               65                               70                               75

GAC GAA GAA ACT GAG AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA      351
Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg
                               80                               85                               90

GAT ACT GTT GAA GAG ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG      396
Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met
                               95                               100                               105

AAA AAC AAG CCA AAG TTC TCA CCA GTT GAT TGA ACCACCACGA      439
Lys Asn Lys Pro Lys Phe Ser Pro Val Asp *
                               110                               115

CTAGTAGATG GTTCAAATGG TGTGCTTTAC ATATAAAAAT AAAGTGTTC      489

TGATGTAAAA AAAAAAAAAA AAAAAAAAAA AACTCGAGAG TATTCTAGAG      539

CGGCCGCGGG CCCATCGTTT TCCACCC      566

```

(2) INFORMATION FOR SEQ. ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Tm 13.17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

Met Lys Leu Leu Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val
  -15                      -10                      -5

Gln Ala Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys
   1                      5                      10

Lys Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala
 15                      20                      25                      30

Arg Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe
 35                      40                      45

Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val
 50                      55                      60

Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu
 65                      70                      75

Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val
 80                      85                      90

Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro
 95                      100                      105                      110

Lys Phe Ser Pro Val Asp *
 115

```

(2) INFORMATION FOR SEQ. ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for Tm 13.17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys
1           5           10           15
Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn
20           25           30
Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val
35           40           45
Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp
50           55           60
Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr
65           70           75           80
Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu
85           90           95
Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe
100          105          110
Ser Pro Val Asp *
115

```

09076348-060704
 102090-81892800

(2) INFORMATION FOR SEQ. ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                -15                      -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA      91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                      1                      5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC      136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
      10                      15                      20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT      181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                      30                      35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA      226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
      40                      45                      50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC      271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
      55                      60                      65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG      316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
      70                      75                      80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT      361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
      85                      90                      95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT      406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
      100                      105                      110

ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTAATA      455
Ile Asp *
      115

TCGTTATGTA AAAAAAAAAA AAAAAA      481

```


(2) INFORMATION FOR SEQ. ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.3

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                -15                      -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA      91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                      1                      5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC      136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
      10                      15                      20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT      181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                      30                      35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA      226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
      40                      45                      50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC      271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
      55                      60                      65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG      316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
      70                      75                      80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT      361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
      85                      90                      95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT      406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
      100                      105                      110

ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA      455
Ile Asp *
      115

TCGTTATGAA AAAAAAAAAA AAAAAAA      482

```

(2) INFORMATION FOR SEQ. ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2, 2.3, and 7.5

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Tm 12.84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
      -15                      -10                      -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
      1                      5                      10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
      35                      40                      45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
      50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
      65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
      80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
95                      100                      105                      110

Phe Ser Pro Ile Asp *
      115

```

(2) INFORMATION FOR SEQ. ID NO: 8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2, 2.3, and 7.5

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for T_m 12.84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
1          5          10          15
Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
20          25          30
Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
35          40          45
Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
50          55          60
Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp
65          70          75          80
Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
85          90          95
Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
100        105        110
Pro Ile Asp *
115

```

09076348-060704

(2) INFORMATION FOR SEQ. ID NO: 9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                -15                      -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA      91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                      1                      5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC      136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
      10                      15                      20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT      181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                      30                      35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA      226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
      40                      45                      50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC      271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
      55                      60                      65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG      316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
      70                      75                      80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT      361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
      85                      90                      95

GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT      406
Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
      100                      105                      110

ATT GAT TAA TTGTTTGTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA      455
Ile Asp *
      115

TCGTTATGTA AAAAAAAAAA AAAAAA      481

```

(2) INFORMATION FOR SEQ. ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Clone 3.4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
 -15 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
 1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp
 95 100 105 110

Phe Ser Pro Ile Asp *
 115

(2) INFORMATION FOR SEQ. ID NO: 11

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for Clone 3.4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
1          5          10          15

Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
20          25          30

Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
35          40          45

Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
50          55          60

Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp
65          70          75          80

Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
85          90          95

Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser
100        105        110

Pro Ile Asp *
115

```

(2) INFORMATION FOR SEQ. ID NO: 12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC      46
          Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                    -15                      -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA      91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
          -5                      1                      5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC      136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val Ser
          10                      15                      20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT      181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
          25                      30                      35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA      226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly
          40                      45                      50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC      271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
          55                      60                      65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG      316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
          70                      75                      80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT      361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
          85                      90                      95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT      406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
          100                      105                      110

ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA      455
Ile Asp *
          115

TCGTTATGAA AAAAAAAAAA AAAAAAA      482

```

(2) INFORMATION FOR SEQ. ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein for Clone 3.9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
  -15                               -10                               -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
   1                               5                               10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15                               20                               25                               30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
 35                               40                               45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50                               55                               60

Val Glu Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu
 65                               70                               75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
 80                               85                               90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
 95                               100                               105                               110

Phe Ser Pro Ile Asp *
 115

```


(2) INFORMATION FOR SEQ. ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 Amino Acids

(B) TYPE: Amino Acid

```
(C) STRANDEDNESS: single
```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Mature protein for Clone 3.9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
1 5 10 15

Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
20 25 30

Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
35 40 45

Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
50 55 60

Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu Val Asp
65 70 75 80

Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
85 90 95

Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
100 105 110

Pro Ile Asp *

(2) INFORMATION FOR SEQ. ID NO: 15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Non-his-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                -15                      -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA      90
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                      1                      5

AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG TCC     136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
      10                      15                      20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT     181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                      30                      35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA     226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
      40                      45                      50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC     271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
      55                      60                      65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG     316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
      70                      75                      80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT     361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
      85                      90                      95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT     406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
      100                      105                      110

ATT GAT TAA TTGTTTTGTA TTTGGCTGAA TTTTGACAAT AAAGGTACTA      455
Ile Asp *
      115

TCGTTATGTA AAAAAAAAAA AAAAAA      481

```

- (2) INFORMATION FOR SEQ. ID NO: 16
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

F02090.04E02860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45 -40 -35	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	
-30 -25 -20	
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT	231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	
-15 -10 -5	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1 5 10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60 65 70	
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	
90 95 100	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105 110 115	
TTTGACTGAA TTTTGACAAT AAAGGTAATA TCGTTATGTA AAAAAAAAAA	645
AAAAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	681

(2) INFORMATION FOR SEQ. ID NO: 17

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
   -55                               -50                       -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
   -40                               -35                       -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
   -25                               -20                       -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
  -10                               -5                        1      5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
   10                               15                       20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
   25                               30                       35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
   40                               45                       50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
   55                               60                       65                       70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
   75                               80                       85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
   90                               95                       100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
  105                               110                       115

```

09676348-060704

- (2) INFORMATION FOR SEQ. ID NO: 18
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
- (ix) FEATURES
- (D) OTHER INFORMATION: His-tagged, signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

(2) INFORMATION FOR SEQ. ID NO: 19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
      -30                      -25                      -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
      -15                      -10                      -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
      1                      5                      10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
     15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
      35                      40                      45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
      50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
      65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
      80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
     95                      100                      105                      110

Phe Ser Pro Ile Asp *
                      115

```

(2) INFORMATION FOR SEQ. ID NO: 20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 682 base pairs

(B) TYPE: nucleic acid

```
(C) STRANDEDNESS: double
```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.3

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, Signal Plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser -55 -50	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -45 -40 -35	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met -30 -25 -20	186
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala -15 -10 -5	231
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser 1 5 10	276
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp 15 20 25	321
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 30 35 40	366
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala 45 50 55	411
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val 60 65 70	456
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val 75 80 85	501
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys 90 95 100	546
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 110 115	595
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA	645
AAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT	682

T049901-060701

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino Acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: no

(vi) ORIGINAL SOURCE:

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(A) LIBRARY: cDNA

(B) CLONE: 2.3

```
(ix)FEATURES
```

(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
105 110 115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

RB125 RT

(2) INFORMATION FOR SEQ. ID NO: 23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.3

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
      -30                      -25                      -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
      -15                      -10                      -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
      1                      5                      10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
     15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
      35                      40                      45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
      50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
      65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
      80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
     95                      100                      105                      110

Phe Ser Pro Ile Asp *
                      115

```

09076348-060704

(2) INFORMATION FOR SEQ. ID NO: 24

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA to mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Tenebrio molitor
 (B) INDIVIDUAL/ISOLATE: none
 (C) CELL TYPE: fat body and whole organism
(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA
 (B) CLONE: 13.17
(ix) FEATURES
 (D) OTHER INFORMATION: His-tagged, Signal plus
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

|                                                             |     |
|-------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG      | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC  | 96  |
| Met Gly Ser Ser His His His His His His Ser                 |     |
| -65 -60 -55                                                 |     |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT | 141 |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly |     |
| -50 -45 -40                                                 |     |
| GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT | 186 |
| Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile |     |
| -35 -30 -25                                                 |     |
| CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC | 231 |
| Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser |     |
| -20 -15 -10                                                 |     |
| CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT | 276 |
| Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile |     |
| -5 1 5                                                      |     |
| GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA | 321 |
| Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly |     |
| 10 15 20                                                    |     |
| GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG | 366 |
| Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu |     |
| 25 30 35                                                    |     |
| GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC | 411 |
| Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn |     |
| 40 45 50                                                    |     |
| GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG | 456 |
| Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu |     |
| 55 60 65                                                    |     |
| AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG | 501 |
| Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu |     |
| 70 75 80                                                    |     |
| AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG | 546 |
| Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu |     |
| 85 90 95                                                    |     |
| ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG | 595 |
| Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys |     |
| 100 105 110                                                 |     |
| TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG    | 643 |
| Phe Ser Pro Val Asp *                                       |     |
| 115                                                         |     |
| TGTGCTTTAC ATATAAAAT AAAGTGTTTC TGATGTAAAA AAAAAAAAAA       | 693 |
| AAAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT      | 743 |
| TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT                    | 777 |

## (2) INFORMATION FOR SEQ. ID NO: 25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

## (ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein with His-tag

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Cys Leu Ile
 -25 -20 -15 -10

Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile
 -5 1 5

Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val
 10 15 20

Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp
 25 30 35

Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly Leu
 40 45 50

Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu Lys Val
 55 60 65 70

Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys
 75 80 85

Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe
 90 95 100

Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser Pro Val Asp *
 105 110 115

```

05876349-060701

- (2) INFORMATION FOR SEQ. ID NO: 26
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 543 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 13.17
  - (ix) FEATURES
    - (D) OTHER INFORMATION: His-tagged; Signal minus
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

|                                                             |     |
|-------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG      | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC  | 96  |
| Met Gly Ser Ser His His His His His His Ser                 |     |
| -30 -25                                                     |     |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT | 141 |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly |     |
| -20 -15 -10                                                 |     |
| GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA | 186 |
| Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys |     |
| -5 1 5                                                      |     |
| CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG | 231 |
| Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser |     |
| 10 15 20                                                    |     |
| CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT | 276 |
| Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp |     |
| 25 30 35                                                    |     |
| CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT | 321 |
| Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly |     |
| 40 45 50                                                    |     |
| CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG AGG GAG | 366 |
| Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu |     |
| 55 60 65                                                    |     |
| AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC | 411 |
| Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile |     |
| 70 75 80                                                    |     |
| ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG | 456 |
| Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val |     |
| 85 90 95                                                    |     |
| TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA | 501 |
| Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser |     |
| 100 105 110                                                 |     |
| CCA GTT GAT TGA CTCGAGCACC ACCACCACCA CCACTGAGAT            | 543 |
| Pro Val Asp *                                               |     |
| 115                                                         |     |



## (2) INFORMATION FOR SEQ. ID NO: 27

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 -30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -15 -10 -5

Gly Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys
 1 5 10 15

Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg
 20 25 30

Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys
 35 40 45

Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val
 50 55 60

Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu
 65 70 75

Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu
 80 85 90 95

Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys
 100 105 110

Phe Ser Pro Val Asp *
 115

```

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: no

(vi) ORIGINAL SOURCE:

(B) INDIVIDUAL/ISOLATE: none

(vii) IMMEDIATE SOURCE:

(B) CLONE: 3.4

(D) OTHER INFORMATION: His-tagged, Signal plus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG          | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC          | 96  |
| Met Gly Ser Ser His His His His His His Ser                     |     |
| -55 -50                                                         |     |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT     | 141 |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly     |     |
| -45 -40 -35                                                     |     |
| GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG     | 186 |
| Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met     |     |
| -30 -25 -20                                                     |     |
| AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT     | 231 |
| Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala         |     |
| -15 -10 -5                                                      |     |
| CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC     | 276 |
| Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser     |     |
| 1 5 10                                                          |     |
| AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC     | 321 |
| Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp     |     |
| 15 20 25                                                        |     |
| AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG     | 366 |
| Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys     |     |
| 30 35 40                                                        |     |
| CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC     | 411 |
| His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala     |     |
| 45 50 55                                                        |     |
| GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG     | 456 |
| Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val     |     |
| 60 65 70                                                        |     |
| GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC     | 501 |
| Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val     |     |
| 75 80 85                                                        |     |
| AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG GTT     | 546 |
| Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Val     |     |
| 90 95 100                                                       |     |
| ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGTA | 595 |
| Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *               |     |
| 105 110 115                                                     |     |
| TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGTA AAAAAAAAAA          | 645 |
| AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT                         | 681 |

09075349 "DEB" 09075349

## (2) INFORMATION FOR SEQ. ID NO: 29

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

## (ix) FEATURES

- (D) OTHER INFORMATION: Precursor protein with His-tag

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
 -25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
 -10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
 10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
 25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
 40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
 55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
 75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
 90 95 100

Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
 105 110 115

```

T02099-04292860

## (2) INFORMATION FOR SEQ. ID NO: 30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (v)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

## (ix) FEATURES

- (D) OTHER INFORMATION: His-tagged, Signal minus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG          | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC      | 96  |
| Met Gly Ser Ser His His His His His His Ser                     |     |
| -30 -25                                                         |     |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT     | 141 |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly     |     |
| -20 -15 -10                                                     |     |
| GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG     | 186 |
| Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln     |     |
| -5 1 5                                                          |     |
| AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG     | 231 |
| Lys Arg Asn Lys Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val |     |
| 10 15 20                                                        |     |
| TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC     | 276 |
| Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp     |     |
| 25 30 35                                                        |     |
| GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT     | 321 |
| Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr     |     |
| 40 45 50                                                        |     |
| GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA     | 366 |
| Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys     |     |
| 55 60 65                                                        |     |
| GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC     | 411 |
| Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile     |     |
| 70 75 80                                                        |     |
| GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT     | 456 |
| Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala     |     |
| 85 90 95                                                        |     |
| TAT GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT     | 501 |
| Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser     |     |
| 100 105 110                                                     |     |
| CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT                | 543 |
| Pro Ile Asp *                                                   |     |
| 115                                                             |     |

## (2) INFORMATION FOR SEQ. ID NO: 31

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
 -30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp  
95 100 105 110

Phe Ser Pro Ile Asp \*  
115

- (2) INFORMATION FOR SEQ. ID NO: 32
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 682 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 3.9
  - (ix) FEATURES
    - (D) OTHER INFORMATION: His-tagged, Signal plus

09875348-060704  
T04090-040904

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

|                                                              |     |
|--------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA              | 50  |
| AGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC    | 96  |
| Met Gly Ser Ser His His His His His His Ser                  |     |
| -55 -50                                                      |     |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT  | 141 |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  |     |
| -45 -40 -35                                                  |     |
| GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG  | 186 |
| Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met  |     |
| -30 -25 -20                                                  |     |
| AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT  | 231 |
| Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  |     |
| -15 -10 -5                                                   |     |
| CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC  | 276 |
| Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser  |     |
| 1 5 10                                                       |     |
| AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC CAA GAG ACG ATC GAC  | 321 |
| Lys Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp  |     |
| 15 20 25                                                     |     |
| AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG  | 366 |
| Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys  |     |
| 30 35 40                                                     |     |
| CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA GTG GCA ACC GAA GCC  | 411 |
| His Val Leu Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala  |     |
| 45 50 55                                                     |     |
| GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG  | 456 |
| Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val  |     |
| 60 65 70                                                     |     |
| GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC  | 501 |
| Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val  |     |
| 75 80 85                                                     |     |
| AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT  | 546 |
| Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys  |     |
| 90 95 100                                                    |     |
| ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGT | 595 |
| Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *            |     |
| 105 110 115                                                  |     |
| TTTGA                                                        | 645 |
| TTTGA                                                        | 682 |



## (2) INFORMATION FOR SEQ. ID NO: 33

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.9

## (ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein with His-tag

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
 -25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
 -10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val
 10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
 25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly Val
 40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
 55 60 65 70

Lys HisVal Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
 75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
 90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
 105 110 115

```



(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino Acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: no

(vi) ORIGINAL SOURCE:

(B) INDIVIDUAL/ISOLATE: none

(vii) IMMEDIATE SOURCE:

(B) CLONE: 3.9

(D) OTHER INFORMATION: Mature Protein with His-tag

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
1 5 10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
35 40 45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp  
95 100 105 110

Phe Ser Pro Ile Asp \*  
115

RB125 RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG          | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC      | 96  |
| Met Gly Ser Ser His His His His His His Ser                     |     |
| -55 -50                                                         |     |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT     | 141 |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly     |     |
| -45 -40 -35                                                     |     |
| GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG     | 186 |
| Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met     |     |
| -30 -25 -20                                                     |     |
| AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT     | 231 |
| Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala     |     |
| -15 -10 -5                                                      |     |
| CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC     | 276 |
| Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser     |     |
| 1 5 10                                                          |     |
| AAA GAG TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC     | 321 |
| Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp     |     |
| 15 20 25                                                        |     |
| AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG     | 366 |
| Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys     |     |
| 30 35 40                                                        |     |
| CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC     | 411 |
| His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala     |     |
| 45 50 55                                                        |     |
| GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG     | 456 |
| Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val     |     |
| 60 65 70                                                        |     |
| GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC     | 501 |
| Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val     |     |
| 75 80 85                                                        |     |
| AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT     | 546 |
| Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys     |     |
| 90 95 100                                                       |     |
| ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGTA | 595 |
| Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *               |     |
| 105 110 115                                                     |     |
| TTTGGCTGAA TTTTGACAAT AAAGGTACTA TCGTTATGTA AAAAAAAAAA          | 645 |
| AAAAAACTCG AGCAACCACCA CCACCACCAC TGAGAT                        | 681 |

## (2) INFORMATION FOR SEQ. ID NO: 37

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 7.5

## (ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein with His-tag

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

```

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
 -25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
 -10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
 10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
 25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
 40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
 55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
 75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
 90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
 105 110 115

```

## (2) INFORMATION FOR SEQ. ID NO: 38

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, Signal minus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

|                                                             |     |
|-------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG      | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC  | 96  |
| Met Gly Ser Ser His His His His His His Ser                 |     |
| -30 -25                                                     |     |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT | 141 |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly |     |
| -20 -15 -10                                                 |     |
| GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG | 186 |
| Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln |     |
| -5 1 5                                                      |     |
| AAA AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG | 231 |
| Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val |     |
| 10 15 20                                                    |     |
| TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC | 276 |
| Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp |     |
| 25 30 35                                                    |     |
| GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT | 321 |
| Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr |     |
| 40 45 50                                                    |     |
| GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA | 366 |
| Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys |     |
| 55 60 65                                                    |     |
| GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC | 411 |
| Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile |     |
| 70 75 80                                                    |     |
| GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT | 456 |
| Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala |     |
| 85 90 95                                                    |     |
| TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT | 501 |
| Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser |     |
| 100 105 110                                                 |     |
| CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT            | 543 |
| Pro Ile Asp *                                               |     |
| 115                                                         |     |

## (2) INFORMATION FOR SEQ. ID NO: 39

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 7.5

## (ix) FEATURES

- (D) OTHER INFORMATION: Mature protein with His-tag

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

```

Met Gly Ser Ser His His His His Ser Ser Gly Leu Val Pro
 -30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
 1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
 95 100 105 110

Phe Ser Pro Ile Asp *
 115

```

09076348-060704



## (2) INFORMATION FOR SEQ. ID NO: 40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Tm 12.84 upper primer with Bam-HI site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CGCGGATCCC TCACCGACGA ACAG

24

## (2) INFORMATION FOR SEQ. ID NO: 41

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5

## (ix) FEATURES

(D) OTHER INFORMATION: Tm 12.84 lower primer with XhoI site

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAGAGGATAA CTAATTGAGC TCGCC 25

09076349-060704

## (2) INFORMATION FOR SEQ. ID NO: 42

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

## (ix) FEATURES

(D) OTHER INFORMATION: Tm 13.17 upper primer with Bam-HI site

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CGCGGATCCC TGACCGAGGC ACAA 24

T04090-05094

## (2) INFORMATION FOR SEQ. ID NO: 43

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Tm 13.17 lower primer with XhoI site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GAGTGGTCAA CTAAGTGGC TCGCC 25

T02090 "04E92050

## (2) INFORMATION FOR SEQ. ID NO: 44

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Consensus of the Tm 12.84 Isoforms

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

|                                                             |     |
|-------------------------------------------------------------|-----|
| GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCN TTC GCC GCC  | 46  |
| Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala                 |     |
| -15 -10                                                     |     |
| ATC GTC ATC GGA GCT CAG GCT CTC ACC GAY GAA CAG ATA CAG AAA | 91  |
| Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys |     |
| -5 1 5                                                      |     |
| AGG AAC AAG ATC AGC AAA GAR TGC CAG CAG GNG TCC GGA GTG TCC | 136 |
| Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser |     |
| 10 15 20                                                    |     |
| CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAY GAT | 181 |
| Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp |     |
| 25 30 35                                                    |     |
| CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG ARA ACT GGA | 226 |
| Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly |     |
| 40 45 50                                                    |     |
| GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC | 271 |
| Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala |     |
| 55 60 65                                                    |     |
| AAG CTG AAG CAT GTG GCC AGC GAC GAA GAR GTG GAC AAG ATC GTG | 316 |
| Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val |     |
| 70 75 80                                                    |     |
| CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT | 361 |
| Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr |     |
| 85 90 95                                                    |     |
| GAC ACC TTC AAG NNT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT | 406 |
| Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro |     |
| 100 105 110                                                 |     |
| ATT GAT TAA TTGTTTTGTA TTTGRCTGAA TTTTGACAAT AAAGGTANTA     | 455 |
| Ile Asp *                                                   |     |
| 115                                                         |     |
| TCGTTATGNA AAAAAAAAAA AAAAAA                                | 481 |

## (2) INFORMATION FOR SEQ. ID NO: 45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

## (ix) FEATURES

- (D) OTHER INFORMATION: Consensus of Seq ID #44 with Tm 13.17

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

GGCANRNNNN AAR ATG AAR YTN CTC TNN TGY YTN RYN TYC NYC RYY 46
 Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
 -15 -10

NTN NTN RTC RNA GYT CAG GCY CTN ACC GAN GNA CAR ATN NAG AAA 91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
 -5 1 5

NNG AAC AAG ATC AGC AAA RAR TGY CAR NAN GNR NNY GGA GTG TCN 136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
 10 15 20

CAA GAG AYN ATN RNC AAA GYY CGC ANN GGT GNC TNG GNN GAY GAT 181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
 25 30 35

CCY AAA NTG AAR NRN CAN GTY YTY TGC NTN NCN ARG ARN RCY GGN 226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
 40 45 50

NTG GCN ACN GAA NCN GGA GAN RYN RNN GTN GAN GTR YTN ARR GNN 271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
 55 60 65

AAG NTG ARG NAN GTN RCY RRC AAC GAC GAA GAR RYN GAN AAR ATC 316
Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile
 70 75 80

RTN NAN AAG TGC GYN GTC AAG ARR GNY ACN NYN GAR GAR ACG GYN 361
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala
 85 90 95

TNY RAY ACY TTC AAR NNT RTY NNN RAN ARY AAR CCN RAN TTC TCN 406
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
 100 105 110

CCN RTT GAT TRA NYNNYYNNNA YTNNGNNNRNR NTTYRANAAT AAAGNNNNTN 458
Pro Ile Asp *
 115

TNRTNNNRNA AAAAAAAAAA AAAAAA 484

```

## (2) INFORMATION FOR SEQ. ID NO: 46

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

## (ix) FEATURES

(D) OTHER INFORMATION: Consensus of Seq ID #45 with B1/B2

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

GGCANRNNNN AAR ATG AAR YTN CTC TNN TGY YTN RYN TYY NYC RYY 46
 Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
 -15 -10

NTN NTN RTC NNA GYT CAG GCY NTN ACY NAN GNA NAN NTN NAG NNA 91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
 -5 1 5

NNG NNC NAR AYC AGC RNA RAR TGY NAR NNN GNR NNY GGA GTG TCN 136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
 10 15 20

NAA GAN RYN ATN RNN ARA GYY CGC ANN GGT GNC TNG GNN GAY GAY 181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
 25 30 35

CCY AAA NTG AAR NNN CAN NTY YTY TGC NTN NYN ARG RNN NYY GRN 226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
 40 45 50

NTR GYN RCN GAA NCN GGA GAN RYN RNN GYN GAN RYR YTN ARR GNN 271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
 55 60 65

AAG NTG ANG NRN NNN NNN RNN ANN RNN RAR RAR RYN RRN ARR NTN 316
Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile
 70 75 80

NYN NRN ARN NNN NNN NNN NNG ARN RNN NYN NNN RAR RNR NNN NNN 361
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala
 85 90 95

TNN RAN NYN YYN AAN NNN NNY NNN RRN ANN ARN CCN RNN TYY TYN 406
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
 100 105 110

CNN RYT RNT TRN NYNNNNNNNN YNNGNNNRNR NTTYRANAAT AAAGNNNYTN 458
Pro Ile Asp *
 115

TNRTNNNRNA AAAAAAAAAA AAAAAA 484

```

- (2) INFORMATION FOR SEQ. ID NO: 47
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.2
  - (ix) FEATURES
    - (D) OTHER INFORMATION: Consensus of Seq. ID #46 with AFP-3
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
|------------|------------|--------|-----|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|
| GGC        | NNR        | NNNN   | AAR | ATG        | AAR        | YTN        | CTC        | YNN | TGY | YTN | RYN | YYY | NYY | RYY | 46  |
|            |            |        |     |            | Met        | Lys        | Leu        | Leu | Leu | Cys | Phe | Ala | Phe | Ala | Ala |
|            |            |        |     |            |            |            | -15        |     |     |     |     |     |     | -10 |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NTN        | NTN        | RYC    | NNR | RYY        | YAN        | GCY        | NTN        | ACY | NAN | RNA | NNN | NNN | NAG | NNR | 91  |
| Ile        | Val        | Ile    | Gly | Ala        | Gln        | Ala        | Leu        | Thr | Asp | Glu | Gln | Ile | Gln | Lys |     |
|            |            | -5     |     |            |            |            | 1          |     |     |     | 5   |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NNG        | NNY        | NAR    | NNC | AGC        | RNN        | RNN        | TGY        | NAR | NNN | GNR | NNY | GGA | GTR | TCN | 136 |
| Arg        | Asn        | Lys    | Ile | Ser        | Lys        | Glu        | Cys        | Gln | Gln | Glu | Ser | Gly | Val | Ser |     |
|            | 10         |        |     |            |            | 15         |            |     |     |     | 20  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NAA        | GAN        | NYN    | NTN | RNN        | ARR        | GYG        | CGC        | ANN | NGT | GNN | NNR | GNN | GAY | GAY | 181 |
| Gln        | Glu        | Thr    | Ile | Asp        | Lys        | Val        | Arg        | Thr | Gly | Val | Leu | Val | Asp | Asp |     |
|            | 25         |        |     |            |            | 30         |            |     |     |     | 35  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| CCY        | AAA        | NTG    | AAR | NNN        | CAN        | NYG        | YTY        | TGC | NTN | NYN | ARG | RNN | NYG | GRN | 226 |
| Pro        | Lys        | Met    | Lys | Lys        | His        | Val        | Leu        | Cys | Phe | Ser | Lys | Lys | Thr | Gly |     |
|            | 40         |        |     |            |            | 45         |            |     |     |     | 50  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NTN        | RYN        | RNN    | GNN | NNN        | GGN        | GAN        | NYN        | NNN | NYN | GAN | NNN | NTN | ARR | RNN | 271 |
| Val        | Ala        | Thr    | Glu | Ala        | Gly        | Asp        | Thr        | Asn | Val | Glu | Val | Leu | Lys | Ala |     |
|            | 55         |        |     |            |            | 60         |            |     |     |     | 65  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| AAR        | NTN        | ANG    | NRN | NNN        | NNN        | RNN        | RNN        | NNN | RAR | RAR | RYN | RRN | RRN | NTN | 316 |
| Lys        | Leu        | Lys    | His | Val        | Ala        | Ser        | Asn        | Asp | Glu | Glu | Val | Asp | Lys | Ile |     |
|            | 70         |        |     |            |            | 75         |            |     |     |     | 80  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NYN        | NNN        | ARN    | NNN | NNN        | NNN        | NNG        | ARN        | RNN | NYN | NNN | NAR | NNN | NNN | NNN | 361 |
| Val        | Gln        | Lys    | Cys | Val        | Val        | Lys        | Lys        | Ala | Thr | Pro | Glu | Glu | Thr | Ala |     |
|            | 85         |        |     |            |            | 90         |            |     |     |     | 95  |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NNN        | RAN        | NYN    | YYN | AAN        | NNN        | NNY        | NNN        | RRN | ANN | ARN | YCN | NNN | TNN | NNN | 406 |
| Tyr        | Asp        | Thr    | Phe | Lys        | Cys        | Ile        | Tyr        | Asp | Ser | Lys | Pro | Asp | Phe | Ser |     |
|            | 100        |        |     |            |            | 105        |            |     |     |     | 110 |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| CNN        | NYN        | RNN    | TRN | NNNNNNNNNN | YNNRNNNNNN | NNNNNNNAAT | AAANNNNNNN |     |     |     |     |     |     |     | 458 |
| Pro        | Ile        | Asp    | *   |            |            |            |            |     |     |     |     |     |     |     |     |
|            | 115        |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
|            |            |        |     |            |            |            |            |     |     |     |     |     |     |     |     |
| NNNNNNNNNA | AAAAAAAAAA | AAAAAA |     |            |            |            |            |     |     |     |     |     |     |     | 484 |



- (2) INFORMATION FOR SEQ. ID NO: 48
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 133 Amino Acids
    - (B) TYPE: Amino Acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: Protein
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE:
  - (ix) FEATURES
    - (D) OTHER INFORMATION: Genral Concensus of Clones,  
B1, B2 and AFP-3

10/09/00 04:29:00

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

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Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
 Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val
 Thr Leu Val
 Val
 -15 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
Tyr Ile Glu Ala Asp Leu Glu Leu Leu Arg Gln Thr Ala
 Thr Pro Arg Lys His Asp
 1 5 10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
Lys Lys Asn Val Ala Glu Asp Ile Leu Thr Arg Ala
Ala Ala Ala Val Ser Lys Asn
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
 Asn Arg Asp Trp Glu Leu Arg Gln Leu Phe
 Lys Glu Glu Met
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 Val Ala Arg Arg Ala Ile Leu Val Ala Ser Glu Ile Glu
 Ile Phe Ala Leu Glu Ile Ile Asp Val Val
 Leu Asn Glu Phe Phe Gln
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser *** Asp Glu
Ala Asp Thr Phe Arg Glu Val Thr Arg Asn Thr Asn Asp Pro
Leu His Ile Thr Phe Arg Lys Ser Asp Asn
 65 70 75

Glu Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro
Lys Ser Glu Asp Leu Ile Glu Asn Thr Glu Asp Val
 Thr Ala
 80 85 90

Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro
Gln Asp Ser Val Phe Glu Val Thr Val Val Leu Lys Asn Arg Ser
 His Ser Ala Asn Phe Met
 His
95 100 105 110

Asp Phe Ser Pro Ile Asp *** *** *
Asn Phe Gly Asp Leu Phe Val *
Lys Val
 115

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